

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 15:27:08 ; Search time 79 Seconds
(without alignments)
211.263 Million cell updates/sec

Title: US-09-924-102-2

Perfect score: 81

Sequence: 1 MLSTHFLFYLFYFLSYSL.....RMGGGGRGGRGTRDGMFLS 81

Scoring table: OLIGO

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SPTREMBL_21.*

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	9.9	135	4	08WYS0
2	8	9.9	151	4	096LUD
3	8	9.9	381	5	076450
4	8	9.9	447	5	09BIV1
5	8	9.9	450	4	096C50
6	8	9.9	485	9	08SC10
7	8	9.9	900	11	09EOX8
8	8	9.9	910	11	09OXC4
9	8	9.9	941	6	09TRA5
10	7	8.6	19	11	006028
11	7	8.6	137	2	09XCQ4
12	7	8.6	137	16	092TF3
13	7	8.6	145	16	09RNG3
14	7	8.6	175	11	09D3N7
15	7	8.6	194	10	09ZUR8
16	7	8.6	195	5	002126

17	7	8.6	214	16	08UFT3	08uft3 agrobacteri
18	7	8.6	244	4	09H700	09h700 homo sapien
19	7	8.6	267	11	09DXX0	09dxx0 mus musculu
20	7	8.6	299	4	096G00	096g00 mus musculu
21	7	8.6	304	3	092194	092194 aspergillus
22	7	8.6	311	5	096200	096200 plasmodium
23	7	8.6	313	8	09MJ02	09mj02 podospora c
24	7	8.6	316	17	08ZVK5	08zvk5 pyrobaculum
25	7	8.6	322	17	09HJ15	09hj15 thermoplas
26	7	8.6	357	10	09LVT8	09lvt8 arabidopsis
27	7	8.6	369	5	09V5V7	09v5v7 drosophila
28	7	8.6	380	4	09UEV7	09uev7 homo sapien
29	7	8.6	381	16	08XBS1	08xbs1 escherichia
30	7	8.6	453	13	087373	087373 gallus gall
31	7	8.6	469	10	08S8A7	08s8a7 arabidopsis
32	7	8.6	478	2	095758	095758 streptomyce
33	7	8.6	504	10	08VUD6	08vud6 arabidopsis
34	7	8.6	507	10	09SKF3	09skf3 arabidopsis
35	7	8.6	519	12	091MK3	091mk3 menangle vl
36	7	8.6	534	10	080853	080853 arabidopsis
37	7	8.6	546	10	004031	004031 arabidopsis
38	7	8.6	581	4	096522	096522 homo sapien
39	7	8.6	581	4	014927	014927 homo sapien
40	7	8.6	583	4	09UJH4	09ujh4 homo sapien
41	7	8.6	606	16	09WJN8	09wjn8 thermotoga
42	7	8.6	607	10	08S3U2	08s3u2 nicotiana b
43	7	8.6	619	4	09NX05	09nx05 homo sapien
44	7	8.6	622	10	09SKF2	09skf2 arabidopsis
45	7	8.6	628	10	09XEM7	09xem7 oryza sativ

ALIGNMENTS

RESULT 1
08WYS0 PRELIMINARY; PRT; 135 AA.
AC 08WYS0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE GLO13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=FROM N.A.
RC TISSUE=LIVER;
RA Liu F., Xu X.R., Qian B.Z., Xiao H., Chen Z., Han Z.;
RT "A novel gene expressed in human liver non-tumor-tissue."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF361491; AL57216.1; -
SO SEQUENCE 135 AA; 15273 MW; 49870F479A2662EA CRC64;

Query Match 9.9%; Score 8; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 SLEDPARL. 26
Db 40 SLGDRARL 47

RESULT 2
096LUD PRELIMINARY; PRT; 151 AA.
AC 096LUD;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ25069 f1s, clone CHL05145.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CEREBELLUM;
 RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
 RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
 RA Kawakami B., Nagai K., Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK037798; BAB1579.1;
 SO SEQUENCE 151 AA; 16915 MW; 99A24D0C477DBF36 CRC64;

Query Match 9.9%; Score 8; DB 4; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.99; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 0;

OY 19 SLGDRRL 26
 Db 48 SLGDRRL 55

RESULT 3

ID 076450 PRELIMINARY; PRT; 381 AA.
 AC 076450;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Spicule matrix protein precursor.
 GN SM37.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidae; Euechinozoa; Echinacea; Echinoidea; Strongylocentrotidae;
 CC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RN RN
 RP SEQUENCE FROM N.A.
 RA Lee Y.-H., Britten R.J., Davidson E.H.;
 RT "SM37, a new skeletogenic gene of the sea urchin embryo isolated by
 RT regulatory target site screening."
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF068737; AAC33762.1;
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00059; Lectin_C.1.
 DR SMART: SM00034; Lectin_C.1.
 DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 KM Matrix protein; Signal.
 FT SIGNAL 1
 FT CHAIN 17
 FT CHAIN 16
 SO SEQUENCE 381 AA; 39136 MW; 62F9320A59BD91A4 CRC64;

Query Match 9.9%; Score 8; DB 5; Length 381;
 Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 0;

OY 64 GGQGGRG 71
 Db 235 GGQGGRG 242

RESULT 4

ID 09BIV1 PRELIMINARY; PRT; 447 AA.
 AC 09BIV1;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Major ampullate spidroin 1 (Fragment).
 GN MASPI.
 OX Argiope aurantia.
 RN [1]

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Araneoidae; Araneidae; Argiope.
 OX NCBI_TaxID=156844;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21179804; PubMed=11283372;
 RA Gately J., Hayashi C., Motriuk D., Woods J., Lewis R.;
 RT "Extreme Diversity, Conservation, and Convergence of Spider Silk
 RT Fibroin Sequences."
 RL Science 291:2603-2605(2001).
 DR EMBL; AF350262; AAK30591.1;
 DR InterPro: IPR000817; P10n.
 DR PRINTS: PR00341; PRION.
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 447 AA; 35630 MW; 78D160B7E6DF24C7 CRC64;

Query Match 9.9%; Score 8; DB 5; Length 447;
 Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 0;

OY 64 GGQGGRG 71
 Db 171 GGQGGRG 178

RESULT 5

ID 096C50 PRELIMINARY; PRT; 450 AA.
 AC 096C50;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical 47.4 kDa protein (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN RN
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC014678; AAH14678.1;
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003066; FN_III.
 DR Pfam: PF00047; fn3.1.
 DR Pfam: PF00047; fn3.1.
 KM Hypothetical protein.
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 450 AA; 47417 MW; 93CEB7844D2C1FB6 CRC64;

Query Match 9.9%; Score 8; DB 4; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 0;

OY 23 RARLCRK 30
 Db 438 RARLCRK 445

RESULT 6

ID 08SC10 PRELIMINARY; PRT; 485 AA.
 AC 08SC10;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Orf6.
 OS Propionibacterium phage phb5.
 OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
 OX NCBI_TaxID=189836;
 RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE-2186396; PubMed-1189111;
RA Chopin M.C., Rouault A., Ehrlich S.D., Gautier M.;
RT "Filamentous Phage Active on the Gram-Positive Bacterium
RT Propionibacterium freudenreichii."
RL J. Bacteriol. 184:2030-2033(2002).
RN [1]
RP SEQUENCE FROM N.A.
RA Chopin M.C., Rouault A., Gautier M.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF428260; AAL31599.1; -
SQ SEQUENCE 485 AA; 48825 MW; 0BAFF44AB3DE91A4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 9; Length 485;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 GGCGGRCG 71
DB 363 GGCGGRCG 370

RESULT 7
O9EOK8 PRELIMINARY; PRT; 900 AA.
ID O9EOK8
AC O9EOK8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HepA-related protein HARP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20313894; PubMed-10857751;
RA Coleman M.A., Eisen J.A., Mohrenweiser H.W.;
RT "Cloning and characterization of HARP/SMART: a prokaryotic Hepa-
RT related SNF2 helicase protein from human and mouse."
RL Genomics 65:274-282(2000).
DR EMBL: AF209773; AAC67648.1; -
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR000330; SNF2_N.
DR Pfam: PF00271; helicase_C.1.
DR Pfam: PF00176; SNF2_N.1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
DR ATP-binding; Helicase.
SQ SEQUENCE 900 AA; 99768 MW; E89EA3783FD4B16F CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 11; Length 900;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 KTKOQKE 37
DB 647 KTKOQKE 654

RESULT 8
O9OYCA PRELIMINARY; PRT; 910 AA.
ID O9OYCA
AC O9OYCA;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HepA-related protein HARP.
GN SMART.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20313894; PubMed-10857751;
RA Coleman M.A., Eisen J.A., Mohrenweiser H.W.;
RT "Cloning and characterization of HARP/SMART: a prokaryotic Hepa-
RT related SNF2 helicase protein from human and mouse."
RL Genomics 65:274-282(2000).
DR EMBL: AF088884; AAF24985.1; -
DR MGD: MGI:1859183; Smartcall.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR000330; SNF2_N.
DR Pfam: PF00271; helicase_C.1.
DR Pfam: PF00176; SNF2_N.1.
DR SMART: SM00490; HELIC; 1.
DR ATP-binding; Helicase.
SQ SEQUENCE 910 AA; 101042 MW; 3F69C87A1B5D8C5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 11; Length 910;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 KTKOQKE 37
DB 647 KTKOQKE 654

RESULT 9
O9TTA5 PRELIMINARY; PRT; 941 AA.
ID O9TTA5
AC O9TTA5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE DNA-dependent ATPase A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-THYMUS;
RX MEDLINE-20179861; PubMed-10713074;
RA Auhuswami R., Truman P.A., Mesner L.D., Hockensmith J.W.;
RT "A Eukaryotic SWI2/SNF2 Domain, an Exclusive Detector of Double-
RT stranded to Single-stranded DNA Transition Elements."
RL J. Biol. Chem. 275:7648-7655(2000).
DR EMBL: AF173643; AAF22285.1; -
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR000330; SNF2_N.
DR Pfam: PF00271; helicase_C.1.
DR Pfam: PF00176; SNF2_N.2.
DR SMART: SM00490; HELIC; 1.
DR ATP-binding; Helicase.
SQ SEQUENCE 941 AA; 104915 MW; AC3309EF813E931B CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 6; Length 941;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 KTKOQKE 37
DB 686 KTKOQKE 693

RESULT 10
O06028 PRELIMINARY; PRT; 19 AA.
ID O06028
AC O06028;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

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DE SQA-2 antigen (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91065311; PubMed=2249652;
 RA Ulker N., Lewis K.D., Hood L.E., Stroyanowski I.;
 RT "Activated T cells transcribe an alternatively spliced mRNA encoding a
 soluble form of Qa-2 antigen.";
 RL EMBL J. 9:3839-3847(1990).
 DR EMBL; X57330; CAA40607.1; -.
 FT NON_TER
 KW Plasmid; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 19 AA; 1956 MW; F2EA894D/5527770 CRC64;

Query Match 8.6%; Score 7; DB 11; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 RMGGGG 68
 Db 6 RMGGGG 12

RESULT 11
 O9XC04 PRELIMINARY; PRT; 137 AA.
 AC O9XC04;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
 DE Hypothetical 15.9 kDa protein.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus
 NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HK695;
 RA Song X.M., Janson H.;
 RT "Different organization and regulation of the glpTQ operons between
 type b and non-typeable Haemophilus influenzae.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF132900; AAD38341.1; -.
 DR InterPro; IPR000620; DUF6.
 DR Pfam; PF00892; DUF6; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 137 AA; 15901 MW; D9678F2624C7891C CRC64;

Query Match 8.6%; Score 7; DB 2; Length 137;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LFTYLF 13
 Db 71 LFTYLF 77

RESULT 12
 O92TF3 PRELIMINARY; PRT; 137 AA.
 AC O92TF3;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Putative plasmid stability protein.
 GN RA1571 OR SMD21651.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid pSymB (megaplasmid 2).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 NCBI_TaxID=382;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021.
 RX MEDLINE=21396508; PubMed=11481431;
 RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
 RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
 RA Golding B., Puehler A.;
 RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
 fixing endosymbiont Sinorhizobium meliloti.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 DR EMBL; AL603647; CAC49970.1; -.
 DR InterPro; IPR002716; PIN.
 DR Pfam; PF01850; PIN; 1.
 KW Plasmid; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 137 AA; 15059 MW; 77EA8989F1734CFD CRC64;

Query Match 8.6%; Score 7; DB 16; Length 137;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 SETLRKT 56
 Db 10 SETLRKT 16

RESULT 13
 O9RRG3 PRELIMINARY; PRT; 145 AA.
 AC O9RRG3;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAY-2002 (TREMblrel. 20, Last annotation update)
 DE Hypothetical protein DR2529.
 GN DR2529.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RI;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eissen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioreistant bacterium Deinococcus
 RT radiodurans RI.";
 RL Science 286:1571-1577(1999).
 DR EMBL; AE002082; AAF12073.1; -.
 DR TIGR; DR2529; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 145 AA; 13709 MW; 4F295FA23E1B4C8 CRC64;

Query Match 8.6%; Score 7; DB 16; Length 145;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 67 GGRGTA 73
 Db 128 GGRGTA 134

RESULT 14
 O9D3N7 PRELIMINARY; PRT; 175 AA.
 AC O9D3N7;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

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DE 5430401F13RIK protein.
GN 5430401F13RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HEAD;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirini L.M., Staudil F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017253; BAB30654.1;
DR MGI; MGI:1918642; 5430401F13RIK.
SQ SEQUENCE 175 AA; 18978 MW; 7DE4B9DAE6AFA4F CRC64;

Query Match 8.6%; Score 7; DB 11; Length 175;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GGCGGRC 70
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Db 107 GGCGGRC 113

RESULT 15
O9ZUR8 PRELIMINARY: PRT: 194 AA.
AC O9ZUR8;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ATG37490 protein.
GN ATG37490.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanden S.E., Umayam L., Talon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
RP SEQUENCE FROM N.A.

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RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RT Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC005896; AAC98065.1;
SQ SEQUENCE 194 AA; 21116 MW; 82485F905192F741 CRC64;

Query Match 8.6%; Score 7; DB 10; Length 194;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 RKTGRKG 60
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Db 146 RKTGRKG 152

Search completed: May 29, 2003, 15:32:37
Job time : 82 secs

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